Introduction report

Bioinformatics is the application of computational technology to handle the rapidly growing repository of information related to molecular biology. Bioinformatics combines different fields of study, including computer sciences, molecular biology, biotechnology, statistics and engineering. It is particularly useful for managing and analysing large sets of data, such as those generated by the fields of genomics and proteomics.

In this report we focus on the bioinformatics tools for mutant analysis through three different projects; mutations in *gai* and *spy* in *Arabidopsis Thaliana*, mutations in *Saccharomyces cerevisiae* and mutations as well as Denovo assembly in *Lactobacillus Helveticus*. We want to sort out new mutation with these tools and learn how to design a bioinformatics test. It includes the quality test, the annotation of our sequenced genomes and various analysis of these results. Thus, everything upstream of the analysis must be properly done, using several software described thereafter. Our machines are too week in order to analyse the data and performed the bioinformatics steps, thus, we will use a cluster dedicated for this lecture, in Bern Switzerland.

**Et sinon, on s’est fait super chier parce que les explications étaient merdiques et que le professeur est pas capable de faire les lignes de codes correspondantes dans son cours et cela m’a énormément rompu la couille. j’en ai marre je me casse.**